

SEARCH REQUEST FORM

a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: 09-14-02

Searcher: Beverly e4979

Terminal time: 20

Elapsed time: _____

CPU time: _____

Total time: 25

Search Site

_____ STIC

_____ CM-1

_____ Pre-S

Type of Search

_____ N.A. Sequence

Vendors

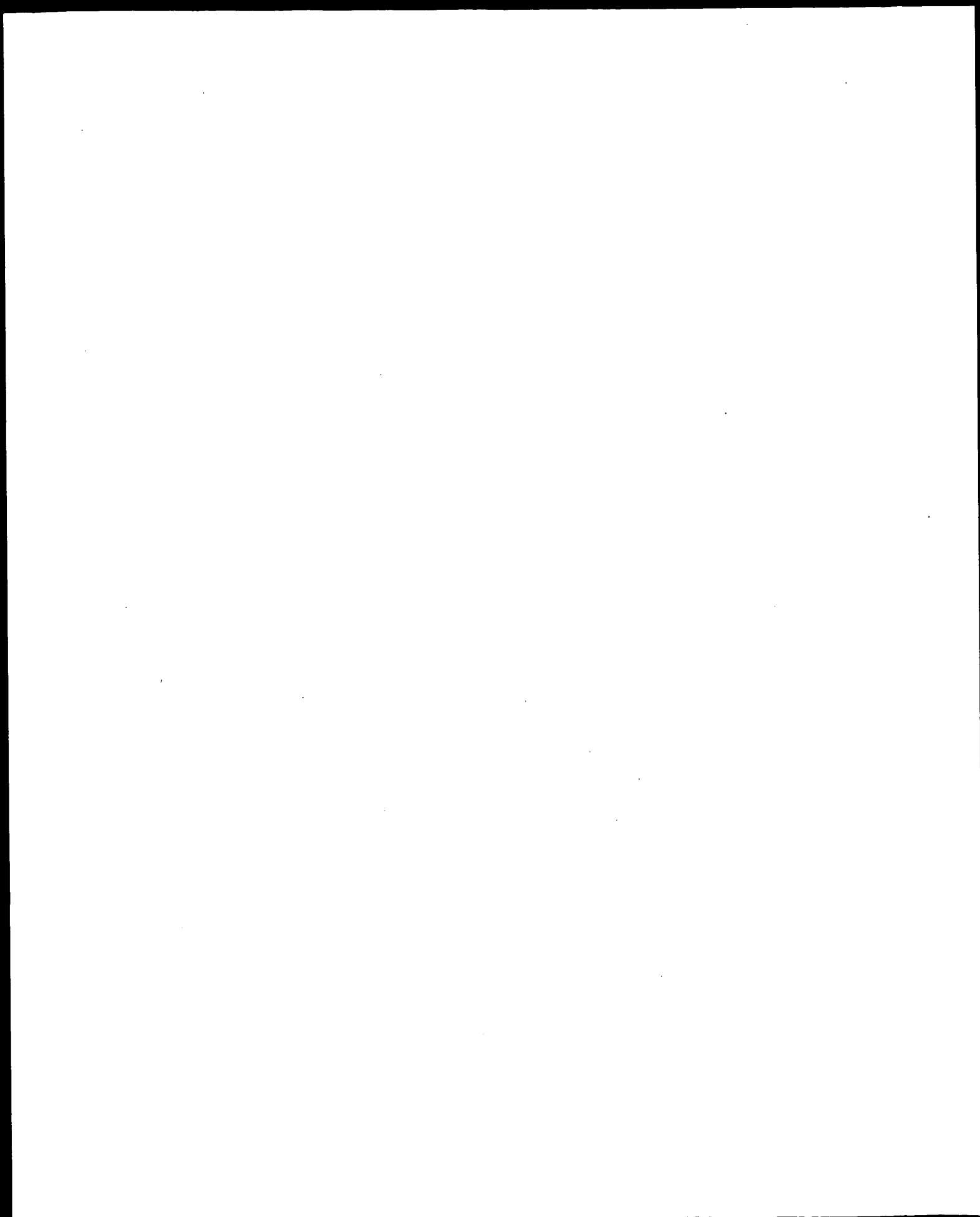
_____ IG Suite

_____ STN

_____ Dialog

_____ APS

_____ Geninfo



GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 10, 2002, 16:50:10 : Search time 4044.31 Seconds

(without alignments)
11455.935 Million cell updates/sec

Title: US-09-843-377-3

Perfect score: 2214
Sequence: 1 gttgactgagcgcgaggtt.....ttgtagtagcagttttt 2214

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

GenBank1.*
1: gb_db.*
2: gb_hg.*
3: gb_in.*
4: gb_cm.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vt.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vt.*
30: em_hgt_hum.*
31: em_hgt_inv.*
32: em_hgt_other.*
33: em_hgtgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
JOURNAL					

1	2214	100.0	2214	9	HSU05875	U05875 Human clone
2	2185.6	98.7	2255	6	ARI68373	ARI68373 Sequence
3	1665.8	75.2	1722	9	BC003624	BC003624 Homo sapi
4	1655.4	74.8	1668	9	HSU05877	U05877 Human clone
5	1537.8	69.5	1566	6	ARI68372	ARI68372 Sequence
6	721	32.6	1255	9	HSU68755	U68755 Human inter
7	716.2	32.3	30438	9	AP000299	AP000299 Homo sapi
8	716.2	32.3	100000	9	AP000045	AP000045 Homo sapi
9	716.2	32.3	100000	9	AP000113	AP000113 Homo sapi
10	716.2	32.3	100000	9	AP000189	AP000189 Homo sapi
11	716.2	32.3	340000	9	AP001717	AP001717 Homo sapi
12	675.4	30.5	56188	9	AP000300	AP000300 Homo sapi
13	538	24.3	552	11	G06755	G06755 human SRS
14	489	22.1	16994	6	AX345890	AX345890 Sequence
15	452.8	20.5	1283	10	S69336	S69336 interferon
16	394	17.8	394	11	G34716	G34716 human SRS
17	378.6	17.1	16994	6	AX345891	AX345891 Sequence
18	99	4.5	1469	10	IFNGRM056	IFNGRM056
19	98.6	4.5	115715	2	AC079411	AC079411 Homo sapi
20	94.4	4.3	1309	10	IFNGRM054	IFNGRM054
21	91.6	4.1	127786	2	AC094129	AC094129 Rattus no
22	91.4	4.1	53552	2	AC100796	AC100796 Homo sapi
23	89.8	4.1	94914	2	AC105592	AC105592 Rattus no
24	89.6	4.0	279090	2	AC091290	AC091290 Mus muscu
25	89	4.0	57544	2	AC103073	AC103073 Rattus no
26	89	4.0	239130	2	AC079420	AC079420 Mus muscu
27	88.8	4.0	182589	2	AC009954	AC009954 Homo sapi
28	88.6	4.0	324	10	IFNGRM055	IFNGRM055
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30	88.2	4.0	217412	2	AC024400	AC024400 Homo sapi
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32	87.8	4.0	86047	2	AC095331	AC095331 Rattus no
33	87.6	4.0	114653	2	AC092411	AC092411 Fells cat
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39	85	3.8	219952	2	AC084804	AC084804 Mus muscu
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ALIGNMENTS

RESULT	1	2214 bp	linear	PRI 24-MAR-1994
HSU05875	Human clone	PSK1 interferon gamma receptor accessory factor-1		
LOCUS	HSU05875	2214 bp	linear	PRI 24-MAR-1994
DEFINITION	(AF-1) mRNA, complete cds.			
ACCESSION	U05875			
VERSION	U05875.1	GI:463549		
SOURCE	human.			
ORGANISM	human sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	Soh, J., Donnelly, R.J., Kotoenko, S., Mariano, T.M., Cook, J.R., Wang, N., Emanuel, S.L., Schwartz, B., Miki, T. and Pestka, S.			
TITLE	Identification and sequence of an accessory factor required for activation of the human interferon gamma receptor			
JOURNAL	Cell 76, 793-802 (1994)			
MEDLINE	94170380			
REFERENCE	2 (bases 1 to 2214)			
AUTHORS	Pestka, S.			
TITLE	Direct Submmission			
JOURNAL	Submitted (01-FEB-1994) Sidney Pestka, UMDNJ-Robert Wood Johnson			

Angel
091843377 Page 1
Sep. 10 3

FEATURES Medical School, 675 Hoes Lane, Piscataway, NJ 08854-5635, USA
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QTL"

sig_peptide 649..729
mat_peptide 730..1659
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GTTAGCTGAGCGGAGGTTGAGTGAGCGGAGTCCGCCACTGCACGCCCTGTTG 60
QY 61 actcgtctcaaaaaaagggagggcgagggagagttgaaagcttaataatgtaactt 120
Db 61 ACTCGCTCAAAAAAAGGGAGGGGCGGCGGAGAGTTGAAAGCTTAATATGTACTT 120
QY 121 tgggggctataagcaaacattcgactaaaggcgaaactcctgaattgtgcgataaa 180
Db 121 TGGGGGCTATTAAACCAACATTTCGACTAAAGGGGGAATCTCCAAATGTGCGATCAA 180
QY 181 gcaaccgaagagaggttgagggggttcagagaggggttcgaaggaagcccgagg 240
Db 181 GCAACCGAGAGAGAGTGGGGGGGCTCAGAGAGGGGTGGGGCTCCAGAGAACCCCGG 240
QY 241 ggcctggcgaggtctcgcgagggcccttcggaaggaatcgcgagcccggaagtgagg 300
Db 241 GGCCTGAGGCGGGGCTCGCGGGGCCCTTCGGAAGGATCGCGGCCCGCGAAGTGGGCG 300
QY 301 tcccgaggggttcagatctcagagacgttcgagaggttcgagctctggagagcgagct 360
Db 301 TCCCGAGGGGCTCAGTCTCCAGAGAGTTCGCGAGAGGCTCCGCGCTCTGGAGGCCGCT 360
QY 361 gctgtgggttcgccgagctgaagcgagagagcccgagagcgaggttcggagagcgag 420
Db 361 GCTGTGGGTCCCGCGCTGAGCGGAGAGGCGCCCGAGGCGCGGCTTCCCGAGAGCGG 420
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Db 421 AAAGTCCGCGCGGCGGGGCTGAGCGGCGGAGAGGCGGCGGCGGCGGCGGCGGCGG 480

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QY 541 tgcgagcctgcgctgcagatgaggggttgaggcgagagtgagaggttcggagagccc 600
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QY 781 caagctctgaggttgaggcgagtgagcgagcgagcgagcgagcgagcgagcgagcgag 840
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QY 841 gtgcagtttaatacacacagagagtaaatggttcacagcgagcgagcgagcgagcgag 900
Db 841 GTGCAGTTTAATACACGAGAGAGTAATGTTTCAAGCGCGAGCATGTCATAGGGGTTG 900
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RESULT 3

BC003624

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

COMMENT

BC003624 1722 bp mRNA linear PRI 12-JUN-2001
Homo sapiens, interferon gamma receptor 2 (interferon gamma transducer 1), clone MGC:2193 IMAGE:2967074, mRNA, complete cds.

BC003624.1 GI:13177681
MGC.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1722)

Strausberg, R.

Direct Submission

Submitted (26-FEB-2001) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>

Contact: MGC help desk

Email: cgapds-remail.nih.gov

Tissue Procurement: ATCC/DCID/DRP

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Institute for Systems Biology

<http://www.systemsbio.org>

contact: amadan@systemsbiology.org

Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia

Greene, Mark Kellerman and Anuradha Madan

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAL Plate: 3 Row: K Column: 17

This clone was selected for full length sequencing because it

passed the following selection criteria: matched mRNA gi: 463551.

location/qualifiers

1.1722

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/db_xref="taxon:9606"

/clone="MGC:2193 IMAGE:2967074"

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/lab_host="DH10B-R"

/note="vector: pOTB7"

126..1139

/codon_start=1

/product="interferon gamma receptor 2 (interferon gamma

transducer 1)"

/protein_id="AAH03624.1"

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QTL"

BASE COUNT

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ORIGIN

Query Match

Best Local Similarity 99.8%; Score 1665.8; DB 9; Length 1722;

Matches 1679; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

532 ggcggccctgcgcgcgcctgcgcctgcgcctgagcgtttggcgcgagcagcgtcc 591

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Db 9 ggcggccctgcgcgcgcctgcgcctgcgcctgagcgtttggcgcgagcagcgtcc 68

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592 ggcggccctgcgcgcgcctgcgcctgcgcctgagcgtttggcgcgagcagcgtcc 651

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RESULT	9
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DEFINITION	Ap000113 100000 bp. DNA linear PRI 25-SEP-1999
ACCESSION	Q78C01-149c3 region, segment 16/20, complete sequence.
VERSION	AP000113
KEYWORDS	AP000113.1 GI:4730847
SOURCE	htc.
ORGANISM	Homo sapiens DNA.
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL	1 (sites)
REFERENCE	Hattori,M., Ishii,K., Toyoda,A., Shiba,T., and Sakaki,Y.
AUTHORS	Homo sapiens 2,051,516bp genomic DNA of 21q22.1 GAT and AML region
JOURNAL	Published Only in Database (1999) In press
REFERENCE	2 (bases 1 to 100000)
AUTHORS	Hirakawa,W., Yamaguchi,H., Imai,K. and Shimada,J.
JOURNAL	Direct Submission
REFERENCE	Submitted (15-APR-1999) to the DDBJ/EMBL/Genbank databases. Mika

COMMENT

This sequence is conducted by Kitasato University JST sequencing laboratory as a JST sequencing team.

Principal Investigator: Yoshiyuki Sakaki Ph.D.
Phone: +81-3-5449-5622, Fax: +81-3-5449-5445,
sakaki@ngc.ims.u-tokyo.ac.jp

Sub-leader: Tadayoshi Shiba Ph.D., Masahira Hattori Ph.D. The sequence is submitted by Human Genome Sequencing in A1S project of JST.

Japan Science and Technology Corporation (JST)
5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081 Japan

For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (<http://www.a1s.tokyo.jst.go.jp/HGS/>) or send email to webmaster@www.a1s.tokyo.jst.go.jp.

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/note="RH17977:The location is between each flanking site
of PCR primers."
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TITLE
JOURNAL

Gardiner, K., Nizetic, D., Francis, F., Lehrach, H., Reinhardt, R. and Yaspo, M.L.

COMMENT

Direct Submission
Submitted (10-Apr-2000) to the DBJ/EMBL/GenBank databases. The Chromosome 21 Mapping and Sequencing Consortium: * RIKEN Genomic Sciences Center, Human Genome Research Group * Institute of Molecular Biotechnology, Genome Analysis * Keio University School of Medicine, Dept. of Molecular Biology * GBF, Dept. of Genome Analysis * Max-Planck Institute for Molecular Genetics (addresses see below)
On May 30, 2000 this sequence version replaced gi:7717331.
The chromosome 21 mapping and sequencing consortium consisting of * RIKEN Genomic Sciences Center, Human Genome Research Group, * Sagami-hara 228-8555, Japan,
* e-mail: hatorigasc.riken.go.jp
* URL: http://hgp.gsc.riken.go.jp/
and
* Institute of Molecular Biotechnology, Genome Analysis, * Beutenbergstrasse 11, D-07745 Jena, Germany,
* e-mail: gscj-submit@genome.imb-jena.de/
* URL: http://genome.imb-jena.de/
and
* Keio University School of Medicine, Molecular Biology, * Tokyo 160-8582, Japan,
* e-mail: nshimizue@mb-med.keio.ac.jp
* URL: http://www.dmb.med.keio.ac.jp/
and
* GBF, Dept. of Genome Analysis,
* Mascherodeg 1, D-38124 Braunschweig, Germany, * e-mail: info.genome@gbf.de
* URL: http://genome.gbf.de/
and
* Max-Planck Institute for Molecular Genetics,
* Ihnestrasse 73, D-14195 Berlin, Germany,
* e-mail: info-chr21@molgen.mpg.de/
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AL163262: Submitted (10-Apr-2000).
Location/Qualifiers

FEATURES

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Job time: 7255 sec

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ALIGNMENTS

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DT	13-FEB-2002 (first entry)	
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KM		Human: chromosome mapping; gene mapping; forensic;
KW		food supplement; medical imaging; diagnostic; genetic disorder; ss.
OS	Homo sapiens.	
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PN	WO200175067-A2.	
PD	11-OCT-2001.	
PE	30-MAR-2001; 2001MO-US08631.	
PR	31-MAR-2000; 2000US-0540217.	
FR	23-MAG-2000; 2000US-0649167.	
PA	(HYSE-) HYSBO INC.	
PI	Drmanac RT, Liu C, Tang YT;	
DR	WPI: 2001-639362/73.	
DR	P-PSDB; ABG12614.	
XX		New isolated polynucleotide and encoded polypeptides, useful in
XT		

PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
PS Claim 1: SEQ ID No 12605; 103bp; English.

XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (II) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp://wipo.int/pub/published_pct_sequences.

XX Sequence 2215 BP: 495 A; 593 C; 628 G; 499 T; 0 other:

Query Match 99.1%; Score 2193.4; DB 23; Length 2215;
Best Local Similarity 99.7%; Pred. No. 0;
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RESULT 2

AA084698 standard; cDNA; 2255 BP.

AA084698;

11-OCT-1995 (first entry)

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Interferon-gamma; AF-1; tumour; ss.

Homo sapiens.

WO9505847-A.

02-MAR-1995.

22-AUG-1994; 94WO-US09438.

20-AUG-1993; 93US-0110119.

(UYNE-) UNIV NEW JERSEY.

Cook JR, Donnely RJ, Emanuel S, Kotenko S, Mariano TM;

Pestka S, Schwartz B, Soh J;

WPI; 1995-106679/14.

P-PSDB; AAR71035.

Suppressing tumours in mammals with accessory factor 1 (AF-1) -

for interferon gamma, specifically induction of class I HLA

antigens, including use of AF-1 DNA in gene therapy

Disclosure; Fig 21B; 114pp; English.

The sequence is that of a cDNA clone encoding human interferon-gamma
 accessory factor-1. Incorporation of AF-1 into immune and tumour
 cells re-establishes normal function with elimination of malignant
 cells.
 See also AA084697-9.
 Sequence 2255 BP; 533 A; 595 C; 628 G; 499 T; 0 other;

Query Match 98.7%; Score 2185.6; DB 16; Length 2255;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 2210; Conservative 0; Mismatches 4; Indels 2; Gaps

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 Db 1 gttagctgagagcgaggttcagtgacgagatcgcgcacatgcatcgaagcctggtg 60
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 QY 61 actccgtctcaaaaaaagggaggggaggggagggaggtgaaagcttaatatgtactt 120
 |||||||
 Db 61 actccgtctcaaaaaaagggaggggaggggagggaggtgaaagcttaatatgtactt 120
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 |||||||
 Db 121 tgggggctattaaagcaaacatttcgactaaaggggagatcctgaaattgtgcataa 180
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 QY 181 gaccccgagagagagatctggggggggtcaggaaggggtgggggtcccaaggaagccggg 240
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 Db 181 gaccccgagagagagatctggggggggtcaggaaggggtgggggtcccaaggaagccggg 240
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 QY 241 ggcctgggacgggggtctcgggggagccctccggaagagatcggggcccgagagtgagcg 300
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 Db 241 ggcctgggacgggggtctcgggggagccctccggaagagatcggggcccgagagtgagcg 300
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 Db 301 tcccgcgggggtccagatctccagagagcttcgggagagctccgctctgggagccggct 360
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 Db 361 gctgggggtcccgcgctgacagcagagagcccccagggcgcggtctcccgagacggg 420
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 Db 421 aaagtcgccgagggggggggtgctgctcggggagcgggggaggggggggggggggggg 480
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 QY 601 gaggggggcccgagcagctgagccgagcggcgagcggcgaggggagcagcagcagcagc 660
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 Db 601 gaggggggcccgagcagctgagccgagcggcgagcggcgaggggagcagcagcagcagc 660
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 QY 661 cggcgtgagtgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 720
 |||||||
 Db 661 cggcgtgagtgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 720
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 QY 721 gacctcttccagctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 780
 |||||||
 Db 721 gacctcttccagctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 780
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 QY 781 caggtcctgaggttggagagcagtgcccttggaggaatgaggaagagagagctgtgtgta 840
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 Db 781 caggtcctgaggttggagagcagtgcccttggaggaatgaggaagagagagctgtgtgta 840
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 QY 841 gtgcagtttaataacacgacagataatggttcaagcggcagatcatgctcataggggtg 900
 |||||||
 Db 841 gtgcagtttaataacacgacagataatggttcaagcggcagatcatgctcataggggtg 900
 |||||||

CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. [AM561497-AM595564](#) represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).
XX
XX Sequence 1781 BP; 436 A; 428 C; 486 G; 430 T; 1 other;

Query Match	49.38;	Score 1090.4;	DB 23;	Length 1781;
Best Local Similarity	87.58;	Pred. No. 1.9e-228;		
Matches 1529; Conservative	0;	Mismatches 147;	Indels 71;	Gaps 28

[illegible]

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Oy	1436	caagaa-gcctttttttctctggtctctgaaataatagaagcccgattaaactggttt--c	149
Db	881	CAGGACCCCTGTTTCTTCTGCTGGCTCTGGAATATATGAGGCGCTGGTTTAAATCCGTTTTTCC	822
Oy	1493	acactccaccaagaatccattaccatagatagaaga--tttaaaagcccaactcaag	154
Db	821	CCCCCTCACCAAGGACATCCCATTTTCCATATAGAAAGAGATATTTTAAAGACCCACTCAG	762
Oy	1549	ccca-ccttaagaagcc-ttgagaagaagcagccaccaaa--gagtagcgtc-tggagctc	160
Db	761	CCCATCTTAAGGCGCTTTTGCCCAAGACACTCCACCAAGGATGACGCTTGGGACTC	702
Oy	1605	tgtgtccattatctcgtttccggaagaagaagaatgtctccaaagccttg--a	166
Db	701	TGTGTCAATATCCCGTTCCTGGAAAAGGACAAAGGATGTCTCCAAACCTTTGTAA	642
Oy	1663	accnaaagatggagctagaccacactgctccctg----aagatcgaagcactgga-gc	171
Db	641	CCAAAAGCATGGGCTGAGCCACCTGCTCCCTCGAAAAATCATCAAGCCCATCGAGGC	582
Oy	1718	tgtatagattctgctc---gagactttcagaagcca-----gattccctttctgccc	176
Db	581	TGCTTAGAGCTTTCGTTTTGAGACTTTCCTCCAGAAACCAAGATTCCTCTTTTGGGGCC	522
Oy	1769	tctaaag-----cctgtcccttgaagacatgagacagcagtgctctcatgaggtg	182
Db	521	TCATAAAAAGGCCCTGTCCTCCACACCATGAGAGAGCGAGCTTCATGCGGGGGA	462
Oy	1821	acaagctttttttttttttttt--ttaagaatttccaaa-----tcaattccagaatga	187
Db	461	CCAAGCTTTTTCATTTTTCCTTAAGAGATTTTCCAAAATATCAAAATCCCAAGATGG	402
Oy	1875	ttttccgagatat-----cccaggaataaag-----ctctcttaaacactaaag	192
Db	401	ATTTTACGGGAGATTTCCCAAGAAAAATTAAGGCTCTCTTTAAACACTMAAAAGGC	342
Oy	1927	catgtaattctgttttagc--aaaatgatatgacacatc--tctgatacttttcat	198
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Oy	1982	tattgttctggagc-tggagagctc--agaagacctgtgtgtc--ctgaatttggcaa--	203
Db	281	TATGTGTTGGGCTTGAAGCTGCAAGAGACCTGCTGCTCTGTGACTTTGGGAACCT	222
Oy	2036	-tgagcggagcccttggggaagtc--acaacactgtccagagaggaacactgagt--	209
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Oy	2092	-ggacctcatgtacatccatgtgtgct--ggcttaaatgttaatactgttaata	214
Db	161	GGGCTTTGATGATACATCCATGAGTGCTCTCGGCTTAAATGATTAATCTGTGAATN	102
Oy	2149	tactctcagaattt--aagatttggttttaactggaataaag--atgtcatagt	220
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Oy	2205	catgttt 2211	
Db	41	CATGTTT 35	
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AC	AAZ20505;		
XT	19-NOV-1999	(first entry)	
DT			
XX			
XX			
DE			
DNAX		Interferon-like receptor subunit 2 coding sequence.	

Db 320 aacacct

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QY	1432	ctggcagaagacctggtttcttcctcgtgctctgtaatatagagcctgatatctaactggttt	1491
Db	440	ctggcgggggtgctgtttcttcctccgtgctgtagatacaaaagcctctgtaatactggttt	499
QY	1492	caagctccaccaagaatccctattacagataagaagatttaagaagcccaactaacgcc	1551
Db	500	caactccgcgaagcaatcccatcaacaatcgaagagatctgaagagaccgagccaagc	559
QY	1552	atcttaagagcctctggacaagacagctcaaccaagaatgaaagctctggagcctctggtcc	1611
Db	560	atcttaagaagccctctggaacaagacagctcaaccaagaatgaaagctctggagcctctggtcc	619
QY	1612	atataccctgcttcgcggaanaagacgaagaatgtttctccaa--cgctcttgaaccaagc	1670
Db	620	gtgtgtgctattccacgaagaagcagaagctgtccccaagaactcttgaaccaaac	679
QY	1671	atggcgcttagcccaacttggtctccctcggaagaagtc---aagcactcgagcgtctagagct	1727
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QY	1787	ggaagcatgtagaacaagcaggtctcactgtgggggtgacaagctttttttttctctc---	1843
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QY	2017	tcgtctgactcttggaatgacgagcgagccctctggcgaggtacacacactgtctccag	2076
Db	1025	ccctctgtatgaagcccccctcgggaga-----cactgtcactgctccagcctgtcccca	1079
QY	2077	cgagggaacactggtgcccctctctgtaactcagatcagtggtgctgctttaaagttaata	2136
Db	1080	gaagggacatttaagtgtgcccctc---tcaataccaacaacacgtggtgaatgtgata	1136
QY	2137	atcctgttaataatacctcctagtaatttaagaatttgtttttaaactcggaatlaaagatt	2196
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ID ABLJ32988 standard; DNA; 16994 BP.			
XX ABLJ32988;			
XX			
XX			
DT 26-MAR-2002 (first entry)			
XX			
DE Human immune system associated gene SEQ ID NO: 961.			
KW Human; immune system disease; cytosine methylation; antileukemic;			

XX	AC	XX	DT	XX	DE	XX	KW
RESULT	7						
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ID	ABL32988	standard; DNA; 16994	BP.				
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DT	26-MAR-2002	(first entry)					
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DE	Human immune system associated gene	SRD	ID NO: 961.				
XX							
KW	Human; immune system disease; cytosine methylation; antiasthmatic;						

SQ Sequence 1233 BP; 326 A; 319 C; 274 G; 314 T; 0 other.

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Oy	1072	ccctcagaacaatctaaagttgccccagaggaaggtccctccatcatcatagttccctc	113
Db	73	ccctcagcagcatctcgggtgagcgaggaagcctccctcatcatcagttccctc	132
Oy	1132	cccttgatcatcgtatcatccccaagcctttttgtttatcttccattactggaa	119
Db	133	cccttcagagccccc--tcccacaacgggctatcttcacagatcatcgtaactaacggaa	139

Oy 1192 aaaggaaggaaatccacacaggtccaaagcccttcaagaagaatccattcatcttgataac 125
 Db 190 aagcgaggaaatccaaaggtttaagctctcttcaagaagaatccatcagtgatgacgc 249
 Oy 1252 ttaaaacctcaagatgtaactgttttaagaatccagacacaaagcttggacaacaaat 1311
 Db 250 ttgagacctaaagaataatcgttttaagaagtgagagcgcctcttcgcacatccgc 309

[illegible]

Qy 1491 tcaactccacaagcatcccatatcagatagaagaagtattttaaaagaccacaactaagc 155

Db 489 tcacttcgcgcgaagcatcccatcacaactcgaagaagtatcttcgaagaaaccgcgaacgc 548

Db 549 taccacagaagccttgacacaagacgtaccacaagaatgctggactggtc 608
QY 1611 cattatctcgtttccggaagaagagcaagaatgcttccaa-cgcttgaaccaag 1660
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127 tc-tgtcggagattccagaagacgatcttcctttgctgccttaaggcgctgcc 178
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 DB 907 gataagattctcttaaacactaaagaacatgtaattctgttagaanaatggtgc 966
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 QY 2136 aatctgtgaataatactcctagtaattttaagatttgtttttaactcgtgaataaagat 219
 DB 1124 agccctgtgaataatgttcacagagatattagcctttttcccccagaattaggaaataaag 118
 QY 2196 tgtatgtacatgcttt 2212
 DB 1184 acctaatatcaactttt 1200

RESULT 5

ID AAQ90808 standard; cDNA; 1283 BP

AAQ90808

XX	
DT	13-NOV-1995 (first entry)

TEN-gamma receptor beta-subunit cDNA

XX
XX
Takes place - seems suspect for both subunit 1, unit 2

KW interferon-gamma-antagonist; ss.

05 Mus sp.

XX	Key	Location/Qualifier
FH		

FT	CDS	FT
----	-----	----

FT	sig_peptide	94..147
EM		/47ac= b

FT	mat_peptide	
148	148	148

XX

MOJ210030-A
PN
XX

15-JUN-1995
PD
XX

PF 07-DEC-1994; 94WO-US14277.
YY

PR 09-DEC-1993; 93US-0164596.

PA (AGUE/) AGUET M.

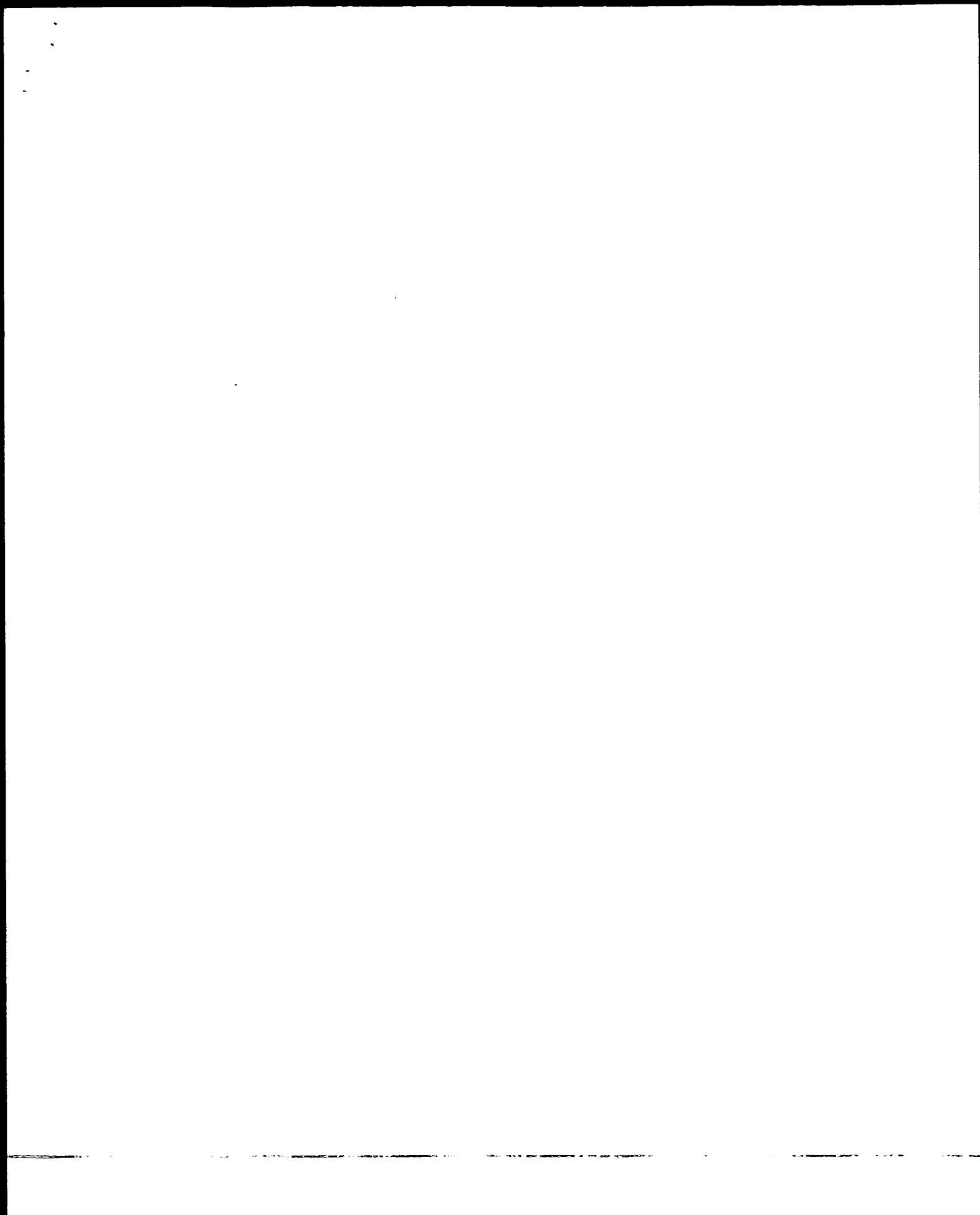
PA (HEMM/) HEMMI S.

XX Aquet M, Boehni R, Hermini S
PI

XX WP.T: 1995-224321/29.
DB

DR P-PSDB; AAR75782

1889 ttgqctgaacatcagaacacctggtcgtctcttgactttggcaatgagccgagccc 2048



GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 10, 2002, 16:52:50 ; Search time 181.1 Seconds
(without alignments)
3002.941 Million cell updates/sec

Title: US-09-843-377-3

Perfect score: 2214
Sequence: 1 gttgactgagcgagcggtt.....ttgtatagtcagttttt 2214

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/prodata/2/ina/5B.COMB.seq:*
3: /cgn2_6/prodata/2/ina/6A.COMB.seq:*
4: /cgn2_6/prodata/2/ina/6B.COMB.seq:*
5: /cgn2_6/prodata/2/ina/PCUS.COMB.seq:*
6: /cgn2_6/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	2185.6	98.7	2255	4 US-08-871-572B-3	Sequence 3, Appl1
2	1537.8	69.5	1566	4 US-08-871-572B-2	Sequence 2, Appl1
3	1173.8	53.0	1197	5 PCT-US94-14277-7	Sequence 7, Appl1
4	452.8	20.5	1283	5 PCT-US94-14277-1	Sequence 1, Appl1
5	68.2	3.1	152331	3 US-09-128-155-16	Sequence 16, Appl1
6	65	2.9	4488	4 US-08-406-030A-3	Sequence 3, Appl1
7	62.8	2.8	319	4 US-09-165-264-8	Sequence 8, Appl1
8	62.8	2.8	320	4 US-09-165-264-7	Sequence 7, Appl1
9	62.8	2.8	320	4 US-09-165-264-11	Sequence 11, Appl1
10	62.6	2.8	4257	2 US-08-690-473-1	Sequence 1, Appl1
11	62.6	2.8	4257	4 US-09-259-821A-1	Sequence 1, Appl1
12	62.6	2.8	4257	4 US-08-458-568A-1	Sequence 11, Appl1
13	62.6	2.8	12001	1 US-08-458-568A-11	Sequence 13, Appl1
14	62.4	2.8	320	4 US-09-165-264-14	Sequence 14, Appl1
15	62	2.8	320	4 US-09-165-264-13	Sequence 12, Appl1
16	61.4	2.8	318	4 US-09-165-264-12	Sequence 12, Appl1
17	61	2.8	4060	4 US-08-308-949A-1	Sequence 7, Appl1
18	60.8	2.7	2517	4 US-09-268-140-7	Sequence 7, Appl1
19	59.6	2.7	2150	2 US-08-318-837-1	Sequence 1, Appl1
20	59.2	2.7	43280	2 US-08-804-227C-1	Sequence 1, Appl1
21	58.6	2.6	4257	2 US-08-690-473-1	Sequence 1, Appl1
22	58.6	2.6	4257	4 US-09-259-821A-1	Sequence 1, Appl1
23	58.6	2.6	4257	4 US-08-843-659-1	Sequence 1, Appl1
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25	57.8	2.6	8438	1 US-07-945-283-1	Sequence 1, Appl1
26	57.6	2.6	1292	4 US-08-483-533-37	Sequence 37, Appl1
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ALIGNMENTS

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	31	56.8	2.6	4403	4	US-09-236-503-1	Sequence 1, Appl1
	32	56.8	2.6	4403	5	PCT-US93-02147A-1	Sequence 1, Appl1
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	36	55.8	2.5	4524	3	US-09-206-537-7	Sequence 7, Appl1
	37	55.8	2.5	4524	4	US-09-430-854-7	Sequence 7, Appl1
	38	55.8	2.5	4403765	4	US-09-103-840A-2	Sequence 2, Appl1
	39	55.2	2.5	801	2	US-08-770-379-16	Sequence 16, Appl1
	40	55.2	2.5	801	4	US-08-757-669A-16	Sequence 16, Appl1
	41	55.2	2.5	801	4	US-09-230-371A-16	Sequence 16, Appl1
	42	54.8	2.5	8438	1	US-07-945-283-1	Sequence 1, Appl1
	43	54.6	2.5	1335	5	PCT-US91-06532-1	Sequence 1, Appl1
	44	54.6	2.5	1941	5	PCT-US91-07635-5	Sequence 5, Appl1
	45	54.4	2.5	2888	4	US-08-765-907A-1	Sequence 1, Appl1

RESULT 1
US-08-871-572B-3
: Sequence 3, Application US/08871572B
: Patent No. 6287653
: GENERAL INFORMATION:
: APPLICANT: Pesicka, Sidney
: APPLICANT: Kotenko, Serguei
: APPLICANT: Soh, Jaemog
: APPLICANT: Donnelly, Robert
: APPLICANT: Mariano, Thomas
: APPLICANT: Cook, Jeffrey
: APPLICANT: Emanuel, Stuart
: APPLICANT: Schwartz, Barbara
: TITLE OF INVENTION: Accessory Factor for Interferon Gamma
: TITLE OF INVENTION: and Its Receptor
: NUMBER OF SEQUENCES: 17
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Richard R. Muccino
: STREET: 758 Springfield Avenue
: CITY: Summit
: STATE: New Jersey
: COUNTRY: USA
: ZIP: 07901
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/871,572B
: FILING DATE: 9-JUNE-1997
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Muccino, Richard R.
: REGISTRATION NUMBER: 32,538
: REFERENCE/DOCKET NUMBER: UMD1-011
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (908) 273-4988
: TELEFAX: (908) 273-4679
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2255 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: unknown
: TOPOLOGY: unknown
: MOLECULE TYPE: DNA (genomic)
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: US-08-871-572B-3

Qy	1900	tgggtcttccttaaacacctaagaagcgtgaatctcctggttagcaaatgagatagac	1959
Db	1264	TAAGGCTTCTCTTAAMACACTAAAAGCATGTAAATCCTTGTAGCAAAATGATATGAC	1332
Qy	1960	acatctcgtatacttttttcattatggttggtcgtagcagtcagaagaacctggtcg	2019
Db	1324	ACATCTCGTACTTTTTCATTATTCGTGGGCTGAGACAGTACAGAACCTGGTGGTG	1383
Qy	2020	tcttgactctggcaaatagccggagcccttgagccagtcacacacacctgtccacaga	2079
Db	1384	TCTTGACTTGGCAAAATAGCGGGAGGCCCTTGGC -AGGTACACAACTGTCCACAGA	1442
Qy	2080	gggaactgagtgcccttcattgatccatcagtggtgctgcgcttaaaatgtataaac	2133
Db	1443	GGGAACCTGAGTGG -CCYTCATGTACATCCCATGAGTGtGCTGGCTTAAATGTAAATTAATC	1501
Qy	2140	tctgaatafataccctcagtaattaaagatcttgctttttaaactcgtgaataaaagatgtga	2195
Db	1502	TGTAAATATATCTAGTAATTTAAAGTTTGTTTTAAACGTGAATAAATAAACATTTGTA	1561
Qy	2200	tagtg 2204	
Db	1562	TAGTG 1566	

RESULT 3
 PCT-US94-14277-7
 : Sequence 7, Application PC/TUS9414277
 : GENERAL INFORMATION:
 : APPLICANT: Aguet, Michel
 : APPLICANT: Bohml, Ruth
 : APPLICANT: Hemmi, Silvio
 : TITLE OF INVENTION: Receptor Subunit Polypeptides
 : NUMBER OF SEQUENCES: 8
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Genentech, Inc.
 : STREET: 460 Point San Bruno Blvd
 : CITY: South San Francisco
 : STATE: California
 : COUNTRY: USA
 : ZIP: 94080
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: patin (genentech)
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: PCT/US94/14277
 : FILING DATE: 07-DEC-1994
 : CLASSIFICATION:
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 08/164596
 : FILING DATE: 09-DEC-1993
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Love, Richard B.
 : REGISTRATION NUMBER: 34,659
 : REFERENCE/DOCKET NUMBER: 866PCT
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 415/225-5530
 : TELEFAX: 415/952-9881
 : TELEX: 910/371-7168
 : INFORMATION FOR SEQ ID NO: 7:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 1197 bases
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear

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Best Local Similarity	99.4%;	Pred. No. 6.7e-266;		

Matches 1178; Conservative 0; Mismatches 7; Indels 0; Gaps 0

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Db	64	ggccggcgagccggcgccgacgacgagccggtgtgtgtgtgtgtgtgtgtgt	123
Oy	688	ggaattctgc	747
Db	124	ggagctttcccgccgcccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc	183
Oy	748	cagagaccgaaagtctgcgtcttacaacgaaagagaggttcctgatttggagcagtgagc	807
Db	184	cagacaccgaaagtctgcgtcttacaacgaaagagaggttcctgatttggagcagtgagc	243
Oy	808	ctgagcaatagcaaggagcctgtgtctatccgagtcaagtttaataacccgaagtaaa	867
Db	244	ctgagcaatagcaaggagcctgtgtctatccgagtcaagtttaataacccgaagtaaa	303
Oy	868	tggtttcagcccgacatcatcctatagagggtgaattgtitacagatcaacgacaagag	927
Db	304	tggtttcagcccgacatcatcctatagagggtgaattgtitacagatcaacgacaagag	363
Oy	928	cttaacttcgtccgc	987
Db	364	cttaacttcgtccgc	423
Oy	988	cgcttcgagctgagcgtggagacatccctgcgtgggtgaaatgacctgtgttcaa	1047
Db	424	cgcttcgagctgagcgtggagacatccctgcgtgggtgaaatgacctgtgttcaa	483
Oy	1048	ccactcgtgaattgacgtgtcgagcctccagaaacattgagttgagcccgaggaaggc	1107
Db	484	ccactcgtgaattgacgtgtcgagcctccagaaacattgagttgagcccgaggaaggc	543
Oy	1108	tcctcatataggttctctctcccttgatcagctgatacctccagagccttttt	1167
Db	544	tcctcatataggttctctctcccttgatcagctgatacctccagagccttttt	603
Oy	1168	tgattatctccatctactgaggaagaaaggaagatcaacagtcaagagcccttcaga	1227
Db	604	tgattatctccatctactgaggaagaaaggaagatcaacagtcaagagcccttcaga	663
Oy	1228	agcaactccattcatgtgataacttaaacctccagagtgtaactgttcaagttccag	1287
Db	664	agcaactccattcatgtgataacttaaacctccagagtgtaactgttcaagttccag	723
Oy	1288	gacaactgcttggagaacaaagtaaacctttaagtcgggagatttaagaaatatct	1347
Db	724	gacaactgcttggagaacaaagtaaacctttaagtcgggagatttaagaaatatct	783
Oy	1348	tgtctagaaacaaatgacagatgctccactgagcttcagaagtcactgactccgtg	1407
Db	784	tgtctagaaacaaatgacagatgctccactgagcttcagaagtcactgactccgtg	843
Oy	1408	ggaacatttcgttctgt	1467
Db	844	ggaacatttcgttctgt	903
Oy	1468	agaagctgatttaatactggtttcaacttcaacgaatcccatcgaagtgaagag	1527
Db	904	agaagctgatttaatactggtttcaacttcaacgaatcccatcgaagtgaagag	963
Oy	1528	taattaaagaccacactcaagccatctttagagcgcttggacaagagacagtcaccaag	1587
Db	964	taattaaagaccacactcaagccatctttagagcgcttggacaagagacagtcaccaag	1023
Oy	1588	gataagcgtctggagacgtctgttcatattctgttccgaaagaagagaagaagatggt	1647
Db	1024	gataagcgtctggagacgtctgttcatattctgttccgaaagaagagaagaagatggt	1083

Oy	1648	cctccaaagcctttagacccaagaatgagccctagccacatgctcccttgaagaataag	1707
Db	1084	ctccaaacgcttgaacccaagaataggccctagccacatgctcccttgaagaataag	1143
Oy	1708	ccatcgagactgctagagttctctctcggacattccagaacacagt	1752
Db	1144	ccatcgagactgctagagttctctctcggacattccagaacacacagt	1188

RESULT 4

```

PCT-US94-14277-1
: Sequence 1, Application PC/TUS9414277
: GENERAL INFORMATION:
: APPLICANT: Aguet, Michel
: APPLICANT: Bohrl, Ruth
: APPLICANT: Hemml, Silvio
: APPLICANT: Hemml, Silvio
: TITLE OF INVENTION: Receptor Subunit Polypeptides
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: palin (genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/14277
: FILING DATE: 07-DEC-1994
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/164596
: FILING DATE: 09-DEC-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Love, Richard B.
: REGISTRATION NUMBER: 34,659
: REFERENCE/DOCKET NUMBER: 866PCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-5530
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1283 bases
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
PCT-US94-14277-1

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Query Match	20.5%;	Score 452.8;	DB 5;	Length 1283;
Best Local Similarity	65.7%;	Pred. No. 5.5e-97;		
Matches 734; Conservative	0;	Mismatches 357;	Indels 27;	Gaps 4

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D	252	CAGCATATACCCAAAGCAAGGCGCTTACCAAGGTGAATATAGCTTACATGATGGCTTGG	311
O	870	gttcacgycgcacatcatgcatataggggtgatgtgtacacagatcatcaagaacagatg	929
D	312	G-----CATAGGTGTGGAGCCGACGACGATACGACATCCACACAGCAAGTG	359
O	930	tgaactacgtccgcacatccctcctcagcagctcccaatgattcaatgtaactcctacg	989
D	360	TGACTTAAACAGAGAGCGGCGCCCTTGAAGCTTTTCCACACCATTCACATGCTCTTGGG	419
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D	420	GGTGGGACCCACAGAGGAAACCTCACATTCCAAAGGGGTGGGCGGACCATTTTACA	479
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D	480	CTATGAGAAATGTACTGTTGGACCTCCGAAAAACATCTCGTGTACCCAGGAAAAGTTG	539
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D	540	CCCTGCTATCACTTCTCCCTCCCTCTTGA-----ATGTTTCCAGGGGACATTTTCA	593
O	1170	ttatatgtccattactatgtggaanaagagaaatccac-----agttcaaaagacctt	1223
D	594	GTATCTGTCTCACTACTGTGGGAAAAGTCAGAAACCCAGACAGAAAGTGTGAAGCTTT	653
O	1224	cagaagcaactcatcttcatctgtgataactttaaaccctccagaatgtatcgttllacaag	1283
D	654	CAGAGCACTCCATTTGTGTGGGCAATGTGAAGCATACAGAGATATTTGTTTCAAAAC	713
O	1284	ccaagcgaactgtcttgtgaaacaaagtaactctcttagatcctggcatttlaagaacat	1343
D	714	TGAGGCACACTGATTTTGGAAAAAATAAAATCCGACACATGGGCTCTTGAGCAATGT	773
O	1344	actctgtcagaanaacaaatggaagatgcctccacgtcagatctgaagaatcctgtatc	1403
D	774	ATCTCTACAGAAACAAACGAAATGCTCTCCGACAGGCTCAGCAAGTCACTCTGATTCC	833
O	1404	cgttggaacatcttgctgtcgtcgtcgtgtcgtgcagagagcctglttctcgttctgaa	1463
D	834	GTTGGGACATTTGCAATTGTGCTGCGCCTCGACGGGCGCCTGTCACCTGTTCTCTCA	893
O	1464	ataatgagccttgataataatcgtgtttaaacctccacaaagcatccatcatcaagtata	1523
D	894	ATACCAAGCCGAGTGAAGTACTGTGTTTGAAGCTTCGCCCAAACTCCGAGAACAAATGCA	953
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D	954	AAGATATCTAAAGACCCAGACACCAATTCATCTGTAGAGTGTGGCAAGAGCGTTCAAC	1013
O	1584	aaagatgtagcttgaggactgtgtccatctcgtcttccgagaanaagagacaaga	1643
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RESULT 5
US-09-128-155-16/c
: Sequence 16, Application US/09128155
: Patent No. 6117654
: GENERAL INFORMATION:
: APPLICANT: Pan, Yang
: TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
: TITLE OF INVENTION: AND USRS THEREOF
: FILE REFERENCE: 09404/052001
: CURRENT APPLICATION NUMBER: US/09/128,155

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RESULT 7

Query Match	2.88;	Score 62.8;	DB 4;	Length 320;
Best Local Similarity	50.38;	Pred. No. 7.2e-06;		
Matches 154; Conservative	0;	Mismatches 152;	Indels 0;	Gaps 0;

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Dd	62	ggaggagggagggagggagggagggagggagggagggagggagggagggagggaggg	122
QY	309	ggatccaaattccaaagaacgtttccggagaggtccaccgcattctggagagccaggtcttgggg	366
Dd	122	ggaggagggagggagggagggagggagggagggagggagggagggagggagggaggg	182
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QY	429	gggcagggagccggtcgccacctgggggacggagacggggcagggcagggcagggcagggcagag	488
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QY	489	ccgaat	494

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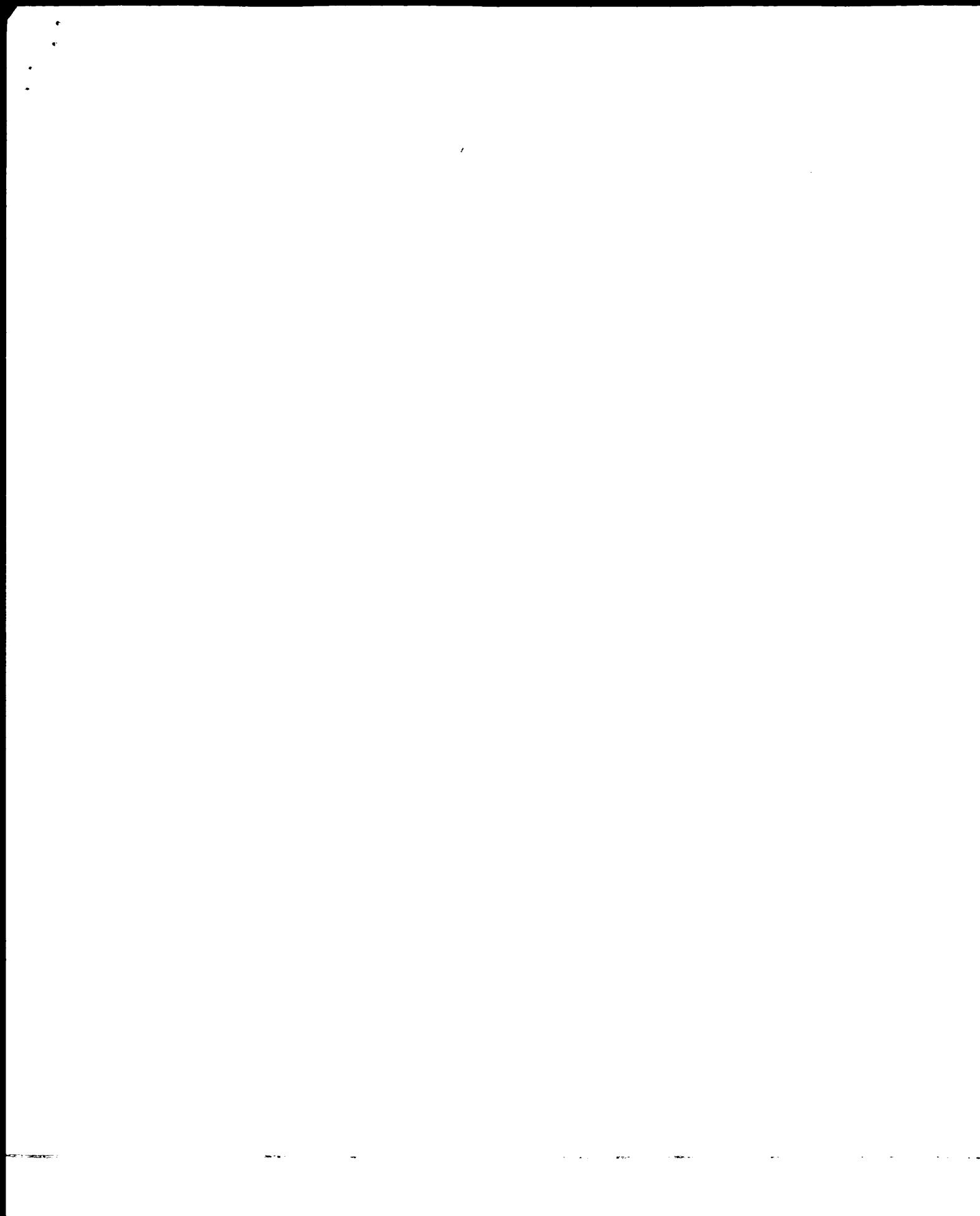
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Db	184 ggg	243				
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OY	487 ag 488					
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Wed Sep 11 09:07:47 2002

us-09-843-377-3.rni

Page 11



GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 10, 2002, 16:43:15 ; Search time 2345.94 Seconds

(without alignments)
12737.861 Million cell updates/sec

Title: US-09-843-377-3

Perfect score: 2214
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 segs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hnc:*
9: gb_estl:*
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13: em_gss_hum:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	979.4	44.2	1035	9	AL576459
3	977	44.1	1044	9	AL563821
4	972	43.9	1059	9	AL571353
5	945.6	42.8	1003	9	AL553183
6	945.8	42.7	959	9	AL542174
7	942.8	42.6	991	9	AL567783
8	937.4	42.3	1013	9	AL567783
9	933.8	42.0	990	9	AL570601
10	929.6	41.8	955	9	AL560745
11	925.2	41.6	969	9	AL582145
12	897.8	40.6	920	9	AL553462
13	896.6	40.5	924	9	AL545745
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16	892.6	40.2	938	9	AL551475
17	890.2	40.2	938	9	AL569290

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19	875.6	39.5	908	9	AL526278
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24	837.6	37.8	881	10	BG749040
25	836	37.7	929	10	B1761952
26	835.6	37.7	862	9	AL539325
27	832.4	37.6	974	10	B1756893
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29	810.6	36.6	829	10	B1761719
30	802.4	36.2	917	10	B1517334
31	798.8	36.1	825	9	AL567425
32	762.2	34.0	930	9	AL551862
33	752	34.0	796	10	BG756460
34	750	33.9	774	9	AL574366
35	749.4	33.8	807	9	AL572349
36	743.4	33.6	1040	10	BE766743
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ALIGNMENTS

RESULT 1
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prime, mRNA sequence.
ACCESSION AL550285
VERSION AL550285.1 GI:12887110
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT
Contact: Genoscope
Genoscope Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

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/clone="CSODI039YC04"
/clone_1lb="LTI_NFL006.PL2"
/tissue="type="Placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
life Technologies. Contact : Peng Liang life technologies,
a division of invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : liliang@life.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 254 a 311 c 257 g 248 t 2 others
ORIGIN

[illegible]

Oy 1090 gtaccccaagagaagcgtccctcatc- atcaggttcctcctccccttgacatcgctga 114
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Db 1057 GGGACCCAGAGAAGGCCCTCATCAAAACAGGKTCCCCCCTTCCTTGACATCGGTGA 998

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Db	997	NACCCCAAGCGGCTTTTXXXTATATATGTGCATTACTGGAAAAAGRGAAAYCAAC	938
Oy	1208	aggtcaaaagcccttcagaagaacctccattcatttgtataacttaaa-ccccga	1266
Db	937	AGGTCAAAAGGCCCTTTCAGAAGAACCTCCATTTCATGTGAATACTTAACACCCCCCAG	878
Oy	1267	gtctactgtttaacaagtcagcgacacactgcgtttggaaaacaaagtlaacatccttagagtc	1326
Db	877	GTTGTAAGTTTTAAGYCCAGGACAACACTGTTTGGAACAAAAGTAACATCTTTGAGATC	818
Oy	1327	gggcattaagcaacatatctctctcagaacaaatggagatagctccactagagcttag	1386
Db	817	GGGCAATTTAAGCAACATWTCTCTCTACGAACAATGGCAGATGGCTCCACTAGAGCTTAG	758
Oy	1387	caaatgcatccctgatctccgttgggaacaatttcgtctgctgctgctgagcagagcctgt	1446
Db	757	CAGATCATCTGTGATCTCGTGGGACAACTTTTCGKGTGCTCGGTCTGGCAGAGACCCTGT	698
Oy	1447	ttcttcttgctctgaatatagagagccgttatgaactgttttaactgttttaacatccagaacg	1506
Db	697	TTCWTTCCGTCTCTGAATAATATAGAGGCCGTGATTAATAACTGG-TTCACTCATCCACAAC	639
Oy	1507	atcccatltaacagatagaagagialttaaaaaaacccaactcagcccatcttagagccttg	1566
Db	638	ATCCCATTTACAGATATGAGAGATATTAAAAAGCCCAACTCACCCATCTTAGAGGCTTG	579
Oy	1567	ggcaagaagacgtcacccaagaagttagcgcgtggagacgtcgtgtccatctactcgtttccg	1626
Db	578	GACAAAGACAGCTCACCAAAGATGACGTCTGGACCTCTGTGCATTATCTGTTTTCCG	519
Oy	1627	gaaaagaagaagaagatgtcttccaaacgctttgaaccaagaacatgagcctagccact	1686
Db	518	GAAAGGACGACAAAGATGTTCTTCACAAAGCTTTTGAACCAAGAGGAGGCTTACGCCACG	459
Oy	1687	ggctcccttggaaagaagataaaccaactcagagcgtctgataagttctgtctcgaacctcaag	1746
Db	458	GGCCCCCGGGAAGATCAACCCACCGGAGCTGCTAAGTTCGCTTGAGACTTCCCAGAG	399
Oy	1747	accagatctcccttctgctgcctctcaaaagcctgtccctcagaacatgagagacaag	1806
Db	398	ACCAGATATCTCTTTGGCTGCCCCCTTAAGAGGCCGCCCGGAGACATGAGAACACAGAG	339
Oy	1807	gctctatgaggagtgacaagccttttttttcttctaagaagatttcaaatccaatic	1866
Db	338	GCTCAGSGGGGAGAACAGCTTTTTTTTTTTCTTAAGAAATTTCAAAATCAAAATTC	279
Oy	1867	cagaatgatttttcvgagatatcccgagaaattaaagctctctcttaaacacataaaag	1926
Db	278	CAGAAATGTTTTACGGANATVTCACAGGAATTAAGGCTCTCTTAACACATTAANAAGG	219
Oy	1927	catgtaactcgtttagcaaaatgtaatagtacacatctctatacttttltcaattg	1986
Db	218	CATGTAATTCGTTGTAGCAAAATAGMATGACACATCTGTGATCTTTTCATTATTG	159
Oy	1987	gttgagctcgagcaatcagaagaacctgtgcgtcctgactttggcacaatgagccggagc	2046
Db	158	GTTGGGCTGAGCAGTACAGAAACCTGTGTGTCTGTGATTTGGCAAAATGACCGGAGGC	99
Oy	2047	cccttggcagagtcacaaacactctccagcgagagacaatgagcgcttcatgtaca	2106
Db	98	CCCTTGGGCAAGTCAACACACTCTCCACGACGAGACACCGAGTGGGCTCTCATGTACA	39
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DEFINITION	AL553183 L1L.NFLD06_P12 Homo sapiens cDNA clone CSDD1073YE14 3		

prime, mRNA sequence.
 ACCESSION AL553183
 VERSION AL553183.1 GI:12892782
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1003)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
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 Location/Qualifiers
 /organism="Homo sapiens"
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 /clone_1ib="LTI_NF1006_PL2"
 /tissue_type="placenta"
 /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 269 a 217 c 235 g 277 t 5 others
 ORIGIN

Query Match 42.88; Score 946.6; DB 9; Length 1003;
 Best Local Similarity 98.78; Pred. No. 4,4e-159;
 Matches 991; Conservative 4; Mismatches 4; Indels 5; Gaps 4;

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 DB 1003 CCGCCAGCCCTTTTGTATATGTCATTCAGGAAAAAGGA-GAATCCAAAGG 945
 OY 1211 tcaagggcccttcagaagaactcatttcattggaacttaaacctccagagtg 1270
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 DB 944 TCAAGGCCCTTTCAGAGCACTCCATTGATTAAGTAACCTTAACCCCTCCAGAGTGT 885
 OY 1271 actgtttacagtcaggaacactgcttctggaacaaagtaacatctttagatcgagg 1330
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 DB 884 ACTGTTTACAAGTCCAGGACAACTGCTTGGAGCAAAAGTAACATCTTGAAGTGGGC 825
 OY 1331 attagaacacatctctgtcgaagaacaaatgagagatgctccacctgaagttagaag 1390
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 DB 824 ATTATGCAACATCTGCTGACGAACATGAGAGTGGCTCCACTAGCTTAGAGAG 765
 OY 1391 tcatctgatctccgttggaaacatcttctgtctgctgctgctgctgctgctgctgct 1450
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 DB 764 TCACTCTGATCTCCGTGGGAACATTTTCGTCGTGGTGGGAGAGAGACCTGTTTC- 704
 OY 1451 tctgtctgaataatagaagcctgattaaatctggtttcaacatcccaagaatcc 1510
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 DB 705 TCTGTCTCTGAATATAGAGGCTGATTAATATCTGG-TTCCACTCCACCAAGCATCC 647
 OY 1511 cattacagatagaagatatttaagaagcccaatccatcttagagagccttgagaa 1570
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 DB 646 CATTACAGATAGAGATATTAAAGACCACTAGCCCACTTAAGGCGCTTGAGACA 587
 OY 1571 aggaagctcaccacaaagatgaagctgagctctgctgctcattatctcgcttcggaaa 1630
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 DB 586 AGACAGCTCACCAAGGATGAGCTGGAGACTGTGTCATTAATCTGCTTCGGGAAA 527

OY 1631 aggaagaaagatgatttcccaacgcttgaaccaagatgaggcttagccatgct 1690
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 DB 526 AGGAGCAAGAGATGCTCTCCAAAGCCTTTAACCAGATGGGCTCAGCCACTGGCT 467
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 DB 466 CCGTGAAGAGATCAACCACTGGAGAGCTGAGAGCTGCTGCTGAGACTTCCAGAGACCA 407
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 DB 406 GATATCCCTTTTGGCTGCTCTAAAGGCTGCTCCGTCGACAGATAGAGACAGAGCT 347
 OY 1811 catggggatgcaagcttt 1870
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 DB 346 CATGGGGGATGACAGC--TTTTTTTTTTTCTTAAGAAATTTTCAAAATTCACAGA 289
 OY 1871 atgatttacgagatataccaggaanaataaggcttctcttaaacactaaaggatg 1930
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 DB 288 ATGATTTACGAGATATCCAGAGAAATTAAGGCGCTCTTAACACTAAAGGCAATG 229
 OY 1931 taattgctgttagcaaatgatatgacacatctgtatcttttttattatgtgtg 1990
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 DB 228 TAATTGCTTTGTACCAAAATGATATGACACATCTCGATCTTTTTCATTTATGTTG 169
 OY 1991 gctgagcagtcagaagacctgctgctgctgctgctgctgctgctgctgctgctgctgct 2050
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 DB 168 GCGTGAAGCAACAAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 109
 OY 2051 tggagagctcacacaacactgctccagagagagacactgagtgcccttatgatcaca 2110
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 DB 108 TGGGCAAGGTCACAAACCTGCTCCAGCAGGAGACRCCGAGTGGCCCTTCATGATCA 49
 OY 2111 tgggtgctgctttaaataatgtaattatctgtgaataatctacc 2154
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 DB 48 TGGTGTGCTGGCTTAATATGATTAATCTGTAATATATCTG 5

RESULT 6
 AL542174
 LOCUS AL542174 LTI_FL002_PL1 959 bp mRNA linear EST 16-FEB-2001
 DEFINITION AL542174 LTI_FL002_PL1 Homo sapiens cDNA clone CS0DE008Yc19 5 prime
 VERSION AL542174
 ACCESSION AL542174
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 959)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
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 Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="CS0DE008Yc19"
 /clone_1ib="LTI_FL002_PL1"
 /lab_host="DH10B"
 /note="Organ: placenta; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with NotI and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL :

Query Match	42.2%;	Score 933.8;	DB 9;	Length 990;
Best Local Similarity	97.7%;	Pred. No. 8.5e-157;		
Matches 970;	Conservative	8;	Mismatches 11;	Indels 4;
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Db 989	ctttttttgtttttgttcattctatctgaggaaaagaagatccacaaggtctaaaggcc	922		
Qy 1221	tttcagaagaactccattcattctatctgataacttaaacctctccagaagtctactgtttca	1280		
Db 931	tttcagaagaactccattcattcattctatctgataacttaaacctctccagaagtctactgtttca	872		
Qy 1281	agtcacagacacacgctcttggagacaagaacacctttagatctggcgatttaagaa	1340		
Db 871	agtcacagacacacgctcttggagacaagaacacctttagatctggcgatttttaagca	812		
Qy 1341	catctctctgctacgaacaatgycagatgacctccactgagcttcaagcaatccctgat	1400		

Db	811	CAATTCCTGCTACGAAACAATGAGCAATCCCTCCACGTGACTTTCAGCAAGTCACCTGAT	752
Oy	1401	ctccgttgagaaacttttcgttgtctgcgcgtgtcgtgcgagaagcccttctctcgtgctc	1460
Db	751	CTCCCTGGGAACATTTTCTGTGCTGTGCGTGTGTGGCAGGAGCCTTCTTTCCTGGTCTCT	692
Oy	1461	gaatataagagcctgataataactcagttcttaacacccaacaagcatccatlaaagat	1520
Db	691	GAATATATGAGGCTCGATTAAATACI - GATTTCACATCCACCAACATCCCATTTACAGAT	633
Oy	1521	agaagatatttaaaagaccactcaagcccatcttagagccttgcagaagacagctc	1580
Db	632	ACAAGAGATTTAAAGACCCAACTAGCCCACTTTGAGAGGCTTGGACAGGACAGCTC	573
Oy	1581	accaaagatgagcgtcttggaactctgtgcatcatctcgtcttcccgaaagaagacaag	1640
Db	572	ACCAAGAGTAGAGCTGTGGAGCTGTGTCACATTATCTGTTTCCGAAAGAGCAAGA	513
Oy	1641	aaatgtcttccaaagccttgaacaaagaatgagccttagcccatcgtctccctgaaga	1700
Db	512	AAATTTCTCCAAAGCTTTTAACAAACATGAGGCTTACCCACTGTGGCTCTCGAAGA	453
Oy	1701	gataaagcactcgagcctgcgtatagttcgtctcgtgacattccagaagacaagatccct	1760
Db	452	GATCAAGCACTGAGAGCTGTAGAGTTTGTGTGAATTTCCAGAGACAGATATTCCTT	393
Oy	1761	tgtcgtccttaaaagcctgtccctgcagagacatgagagaacagcagttccatgggggtg	1820
Db	392	TTCGCTGCTTAAAGGCGCTTCCCTCGACATGAGACAGCAGGCTTCATAGGGGGGTG	333
Oy	1821	acaaagcttttttttttttttcttaagaacttttcaaatcaaatccagaatgatattac	1880
Db	332	ACAAGC - TTTTTCCTTAAAGAAATTTTCAAAATCAAAATCCAGATGATTATAC	274
Oy	1881	ggagatgccaggaanaattagagcttctctaacaactaaaagacatgataatgtctg	1940
Db	273	GGAGATATCCAGGAAATTAAGGCTTCTTTAAACCTTAAAGGCAATTAATATGCTTG	214
Oy	1941	ttagaanaatgagatagacacatctcgtacttttcatatattggttggctgaagag	2000
Db	213	TTAGCAAAATGATATGACACATCTGTATCTTTTTCATTATGTTGGTGGCTGACAG	154
Oy	2001	ttagaagaacctgctcgtctcgtctgactttggcaatgagcggagagcccttggcagctc	2060
Db	153	TCAGAGAGCTGTGCTGTCTTTGACTTTGGCAATATAGCCGAAACCCCTTGGGCAAGTTC	94
Oy	2061	acacaactctgccacgagaggaactgagtgagcccttaatgatacacaatggttggctg	2120
Db	93	ACACAACTGTCCACGACGAGGACMCCTGAGTGCGCCCTCATGTATACATCAATGGTGCTK	34
Oy	2121	gcttaaaatgataataactctgttaaatatctc 2153	
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RESULT	10
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LOCUS	
DEFINITION	Al560745 955 bp mRNA linear EST 16-FEB-2001
VERSION	Al560745.LTI.NF010_EC2 Homo sapiens cDNA clone CSDD004RH09 5
ACCESSION	Al560745
KEYWORDS	prime, mRNA sequence.
SOURCE	Al560745.1 GI:12907500
ORGANISM	EST.
REFERENCE	human.
AUTHORS	Homo sapiens
TITLE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
JOURNAL	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
COMMENT	1 (bases 1 to 955)
	I.I.M.B., Gruber C., Jessee J. and Polayes D.
	Unpublished cDNA libraries and normalization
	Contact: Genoscope - Centre National de Sequencage

Query Match	40.4%;	Score 895;	DB 9;	Length 931;
Best Local Similarity	99.1%;	Pred. No. 7.1e-150;		
Matches 927; Conservative	4;	Mismatches 0;	Indels 4;	Gaps 3

